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          RAW SEQUENCE LISTING              DATE: 05/04/2000
          PATENT APPLICATION:  US/09/553,431    TIME: 16:30:29

          Input Set : A:\Un900411.app
          Output Set: N:\CRF3\05042000\I553431.raw

     3  <110> APPLICANT: Osteryoung, Katherine W.
     5  <120> TITLE OF INVENTION: Manipulation of Min Genes in Plants
     7  <130> FILE REFERENCE: 920905.90041
C--> 9  <140> CURRENT APPLICATION NUMBER: US/09/553,431
C--> 10 <141> CURRENT FILING DATE: 2000-04-19
     12 <150> PRIOR APPLICATION NUMBER: 60/130,403
     13 <151> PRIOR FILING DATE: 1999-04-19
     15 <160> NUMBER OF SEQ ID NOS: 4
     17 <170> SOFTWARE: PatentIn Ver. 2.1
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 978
     21 <212> TYPE: DNA
     22 <213> ORGANISM: Arabidopsis thaliana
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     33 cca tca tct ctc tca caa aag act cta ata tct tca cca aga ttc gtc   96
     34 Pro Ser Ser Leu Ser Gln Lys Thr Leu Ile Ser Ser Pro Arg Phe Val
     35              20                  25                  30
     37 aat aac cct agc aga cgg agt cca ata cga tcc gtt ctt caa ttt aat  144
     38 Asn Asn Pro Ser Arg Arg Ser Pro Ile Arg Ser Val Leu Gln Phe Asn
     39          35                  40                  45
     41 cgc aaa ccg gaa ctc gcc gga gaa acg ccg cgt atc gtc gtt atc acc  192
     42 Arg Lys Pro Glu Leu Ala Gly Glu Thr Pro Arg Ile Val Val Ile Thr
     43      50                  55                  60
     45 tcc gga aaa ggc ggt gtt gga aag acg aca acc acc gca aat gtc ggt  240
     46 Ser Gly Lys Gly Gly Val Gly Lys Thr Thr Thr Thr Ala Asn Val Gly
     47  65                  70                  75                  80
     49 ctc tct ctc gct cgt tac ggt ttc tca gtt gtc gcc att gac gcc gac  288
     50 Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp
     51              85                  90                  95
     53 ctt ggt ctc cgt aac ctc gat ctc ctc cta ggg tta gag aat cga gtc  336
     54 Leu Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val
     55              100                 105                 110
     57 aat tac act tgc gtc gag gtt ata aac gga gat tgt cgt ctc gat caa  384
     58 Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln
     59          115                 120                 125
     61 gct ctg gta cgt gat aag cgt tgg tcg aat ttc gaa ttg cta tgt ata  432
     62 Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile
     63      130                 135                 140
     65 tct aaa cct aga tcg aaa ctt ccg atg gga ttt ggt ggt aaa gca ttg  480
     66 Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu
     67 145                 150                 155                 160
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 69 gaa tgg ctt gtg gat gcg ttg aaa act aga ccg gaa ggt tca ccg gat    528
 70 Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp
 71             165                 170                 175
 73 ttc atc atc atc gat tgt cct gca gga atc gat gcc gga ttc ata acc    576
 74 Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr
 75             180                 185                 190
 77 gcc att act ccg gcg aat gaa gca gtt ctg gta aca act ccg gat ata    624
 78 Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile
 79             195                 200                 205
 81 aca gcg tta agg gat gct gat agg gtt acg ggt ttg tta gaa tgc gat    672
 82 Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp
 83     210                 215                 220
 85 gga atc aga gat ata aag atg att gtg aac aga gtg aga act gat atg    720
 86 Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met
 87 225                 230                 235                 240
 89 att aaa gga gag gat atg atg tca gtg tta gat gtg cag gag atg ttg    768
 90 Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu
 91             245                 250                 255
 93 gga ttg tca ttg ctt ggt gta att cct gaa gat tct gag gtt att cga    816
 94 Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg
 95             260                 265                 270
 97 agc acg aat cga ggg ttt ccg ctt gtt ctg aat aag cct cct acg ctt    864
 98 Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu
 99     275                 280                 285
101 gcg gga ttg gcg ttt gag cag gcg gct tgg aga ctc gtt gag caa gat    912
102 Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp
103     290                 295                 300
105 agt atg aag gct gtt atg gtg gag gaa gaa cct aag aaa cgt ggc ttc    960
106 Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly Phe
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124             20                  25                  30
126 Asn Asn Pro Ser Arg Arg Ser Pro Ile Arg Ser Val Leu Gln Phe Asn
127         35                  40                  45
129 Arg Lys Pro Glu Leu Ala Gly Glu Thr Pro Arg Ile Val Val Ile Thr
130     50                  55                  60
132 Ser Gly Lys Gly Gly Val Gly Lys Thr Thr Thr Thr Ala Asn Val Gly
133  65                  70                  75                  80
135 Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp
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136                     85                    90                      95
138 Leu Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val
139             100                 105                 110
141 Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln
142         115                 120                 125
144 Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile
145     130             135                 140
147 Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu
148 145             150                 155                 160
150 Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp
151             165                 170                 175
153 Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr
154         180                 185                 190
156 Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile
157         195                 200                 205
159 Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp
160     210             215                 220
162 Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met
163 225             230                 235                 240
165 Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu
166             245                 250                 255
168 Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg
169             260                 265                 270
171 Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu
172         275                 280                 285
174 Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp
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178 305             310                 315                 320
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187 <212> TYPE: DNA
188 <213> ORGANISM: Tagetes erecta
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191 <221> NAME/KEY: CDS
192 <222> LOCATION: (50)..(934)
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196                                                        Met Thr Ser
197                                                          1
199 ctg agg ttt cta aca gaa ccc tca ctt gta tgc tca tcc act ttc ccc   106
200 Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser Thr Phe Pro
201     5               10              15
203 aca ttc aat ccc cta cac aaa acc cta act aaa cca aca cca aaa ccc   154
204 Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr Pro Lys Pro
205   20              25              30                  35
207 tac cca aag cca cca cca att cgc tcc gtc ctt caa tac aat cgc aaa   202
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208 Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr Asn Arg Lys
209             40              45              50
211 cca gag ctc gcc gga gac act cca cga gtc gtc gca atc gac gcc gac   250
212 Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile Asp Ala Asp
213             55              60              65
215 gtt ggt cta cgt aac ctc gat ctt ctc ggt ctc gaa aac cgc gtc       298
216 Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val
217             70              75              80
219 aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga ctc gac caa   346
220 Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg Leu Asp Gln
221             85              90              95
223 gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg ctt tgt att   394
224 Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile
225 100             105             110             115
227 tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga aaa gct tta   442
228 Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly Lys Ala Leu
229             120             125             130
231 gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc ccg gat ttt   490
232 Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys Pro Asp Phe
233             135             140             145
235 ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc ata acc gcc   538
236 Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr Ala
237             150             155             160
239 att aca ccg gct aac gaa gcc gta tta gtt aca aca cct gat att act   586
240 Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile Thr
241     165             170             175
243 gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa tgt gat gga   634
244 Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp Gly
245 180             185             190             195
247 att agg gat att aaa atg att gtg aac aga gtt aga act gat ttg ata   682
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249             200             205             210
251 agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag atg ttg gga   730
252 Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu Gly
253             215             220             225
255 ttg tca ttg ttg agt gat acc cga gga ttc gaa gtg att cgg agt acg   778
256 Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile Arg Ser Thr
257             230             235             240
259 aat aga ggg ttt ccg ctt gtg ttg aac aag cct ccg act tta gca gga   826
260 Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu Ala Gly
261     245             250             255
263 ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa gat agc atg   874
264 Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp Ser Met
265 260             265             270             275
267 aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga ttt ttc tcg   922
268 Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly Phe Phe Ser
269             280             285             290
271 ttt ttt gga ggt tagtgatcga attcgttgaa tcgttgagtt gggtttgttt       974
272 Phe Phe Gly Gly
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275 tggtggagaa atgtgtcttg tttgttcatg taggagctgc tatgtgtcac ttgaaatgtt 1034
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285 <211> LENGTH: 295
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294              20                  25                  30
296 Pro Lys Pro Tyr Pro Lys Pro Pro Ile Arg Ser Val Leu Gln Tyr
297          35                  40                  45
299 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
300      50                  55                  60
302 Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Gly Leu Glu
303  65                  70                  75                  80
305 Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
306              85                  90                  95
308 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
309              100                 105                 110
311 Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly
312          115                 120                 125
314 Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys
315      130                 135                 140
317 Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe
318 145                 150                 155                 160
320 Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Leu Val Thr Thr Pro
321              165                 170                 175
323 Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu
324          180                 185                 190
326 Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr
327          195                 200                 205
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335 Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr
336              245                 250                 255
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339          260                 265                 270
341 Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly
342          275                 280                 285
344 Phe Phe Ser Phe Phe Gly Gly
345      290                 295
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Input Set : A:\Un900411.app
Output Set: N:\CRF3\05042000\I553431.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date